

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

SCHMIDT, Harald
 ZABEL, Ulrike
 POLLER, Wolfgang

(ii) TITLE OF THE INVENTION: Isolated and purified human soluble
 guanylyl cyclase α1/β1 (hsGCa1/β1)

(iii) VOS-101

(iv) US 09/762,767
 2001-02-13

(iv) PCT/DE99/02601
 1999-08-16

(iv) DE 198 37 015.6
 1998-08-14

(v) NUMBER OF SEQUENCES: 10

(vi) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) DATA TO SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3015 basepairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: doublestrand
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCTTATGGC	GATTGGCGG	CTGCAGAGAC	CAGGA	CTAGTCTGAG	60
CCTAGGGGT	GGGACTCAGC	TCAGAGTCAG	TTTCCAGAA	GTGAGGTTCA	120
TTCCTACACT	TTCCCTGCGC	TAGAGCAGCG	AGCAGCCTGG	AACAGACCCA	180
ACCTGTGGGG	GAGGGAGCGC	CTGGAGGAGC	TTAGAGACCC	CAGCCGGCG	240
ATGTGCGGAT	TTGCGAGGCG	CGCCCTGGAG	CTGCTAGAGA	TCCGGAAGCA	300
GTGTGCGAAG	CCACCAAGAC	TGCGGCTCTT	GGAGAAAGCG	TGAGCAGGGG	360
TCTCCGCGCC	TGTCTGCACC	CTGTCGCTG	AGCTGCCTGA	CAGTGACAAT	420
TTACCAAGTGT	CCTTGAAATTG	ATAGTGGCTT	CTGTTGTCA	GTCTCATATA	480
CTCATCAGGA	GGAGATCGCA	GCAGGGTAAG	AGACACCAAAC	ACCATGTTCT	540
CAAGGATCTC	AAGATCACAG	GAGAGTGTCC	TTTCTCCTTA	CTGGCACCCAG	600
TAACGAGTCT	TCAGAGGAGG	CAGCAGGAAG	CTCAGAGAGC	TGCAAAGCAA	660
CTGTCAGAGAC	ATTCTGAGA	AGAACATACA	AGAAAAGTCTT	CCTCAAAGAA	720
GAGCCGAGTC	TATCTTCACA	CTTGGCAGA	GAGTATTGTC	AAACTGATT	780
TGAACGGCTG	AATGTTGCAC	TTCAGAGAAC	ATTGGCAAAG	CACAAAATAA	840
GAAATCTTG	GAAAGAGAAC	ACTTTGAAAA	AACAAATTGCA	GAGCAAGCAG	900
AGTTCCAGTG	GAGGTTATCA	AAGAATCTCT	TGGTGAAGAG	TTTTTAAAAA	960
GGAAGATGAA	AACATCCTTG	GGGTGGTTGG	AGGCACCCCTT	AAAGATTTTT	1020
CAGTACCCCTT	CTGAAACAGA	GCAGCCATTG	CCAAGAACGA	GGAAAAAGGG	1080
GGACGCCCTCC	ATTCTATGCC	TGGATAAGGA	GGATGATT	CTACATGTT	1140
CCCTAACAGAGA	ACCACCTCCC	TGATTCTCC	CGGCATCATA	AAGGCAGCTG	1200
ATATGAAACG	GAAGTGGAAAG	TGTCGTTAAT	GCCTCCCTGC	TTCCATAATG	1260
GTTCGTGAAT	CAGCCCTACT	TGTTGTACTC	CGTTCACATG	AAAAGCACCA	1320
GTCCCCCAGC	AAACCCAGT	CCTCGCTGGT	GATTCCCACA	AGCCATCCCT	1380

	TCCATTCCAT	TTCATGTTG	ACAAAGATAT	GACAATTCTG	CAATTGGCA	ATGGCATTGAG	1440
	AAGGCTGATG	AACAGGAGAG	ACTTCAAGG	AAAGCCTAAT	TTTGAAGAAT	ACTTTGAAT	1500
	TCTGACTCCA	AAAATCAACC	AGACGTTAG	CGGGATCATG	ACTATGTTGA	ATATGCAGTT	1560
	TGTTGTACGA	GTGAGGAGAT	GGGACAAC	TGTGAAGAAA	TCTTCAGGG	TTATGGACCT	1620
5	CAAAGGCCAA	ATGATCTACA	TTGTTGAATC	CAGTGCAATC	TTGTTTTGG	GGTCACCCCTG	1680
	TGTGGACAGA	TTAGAACGATT	TTACAGGACG	AGGGCTCTAC	CTCTCAGACA	TCCCCATTCA	1740
	CAATGCACTG	AGGGATGTGG	TCTTAATAGG	GGAACAAGCC	CGAGCTCAAG	ATGGCCTGAA	1800
	GAAGAGGCTG	GGGAAAGCTGA	AGGCTACCC	TGAGCAAGCC	CACCAAGCCC	TGGAGGAGGA	1860
10	GAAGAAAAAG	ACAGTAGACC	TTCTGTGCTC	CATATTTCCC	TGTGAGGTTG	CTCAGCAGCT	1920
	GTGGCAAGGG	CAAGTTGTGC	AAGCCAAGAA	GTTCAGTAAT	GTCACCATGC	TCTTCTCAGA	1980
	CATCGTTGGG	TTCACTGCCA	TCTGCTCCC	GTGCTCACCG	CTGCAGGTCA	TCACCATGCT	2040
	CAATGCACTG	TACACTCGCT	TCGACCAGCA	GTGTGGAGAG	CTGGATGTCT	ACAAGGTGGA	2100
	GACCATTGGC	GATGCCTATT	GTGTAGCTGG	GGGATTACAC	AAAGAGAGTG	ATACTCATGC	2160
15	TGTTCAAGATA	GCGCTGATGG	CCCTGAAGAT	GATGGAGCTC	TCTGATGAAG	TTATGTCTCC	2220
	CCATGGAGAA	CCTATCAAGA	TGCGAATTGG	ACTGCACTCT	GGATCAGTTT	TTGCTGGCGT	2280
	CGTTGGAGTT	AAAATGCCCC	GTAACTGTCT	TTTTGGAAAC	AATGTCACTC	TGGCTAACAA	2340
	ATTTGAGTCC	TGCAGTGTAC	CACGAAAAT	CAATGTCAGC	CCAACAAC	ACAGATTACT	2400
	CAAAGACTGT	CCTGGTTTCG	TGTTTACCCC	TCGATCAAGG	GAGGAAC	TTC CACCAAAC	2460
20	CCCTAGTGAA	ATCCCCGGAA	TCTGCCATT	TCTGGATGCT	TACCAACAAG	GAACAAAC	2520
	AAAACCATGC	TTCCAAAAGA	AAGATGTGGA	AGATGGCAAT	GCCAATT	TAGGCAAAGC	2580
	ATCAGGAATA	GATTAGCAAC	CTATATACCT	ATTATAAGT	CTTGGGGTT	TGACTCATTG	2640
	AAGATGTGTA	GAGCCTCTGA	AAGCACTTA	GGGATTGTAG	ATGGCTAAC	AGCAGTATT	2700
	AAATTTCAAG	AGCCAAGTCA	CAATCTTCT	CCTGTTAAC	ATGACAAAAT	GTACTCACT	2760
	CAGTACTTCA	GCTCTTCAAG	AAAAAAAAAA	AAACCTAAA	AAGCTACT	TGTGGGAGTA	2820
25	TTTCTATTAT	ATAACCAGCA	CTTACTACCT	GTACTCAAA	TTCAGCACCT	TGTACATATA	2880
	TCAGATAATT	GTAGTCAATT	GTACAAACTG	ATGGAGTCAC	CTGCAATCTC	ATATCCTGGT	2940
	GGAATGCCAT	GGTTATTAAA	GTGTGTTGT	GATAGTGTGCG	TCAAAAAAAA	AAAAAAA	3000
	AAAAAAAAAA	AAAAAA					3015

30

(2) DATA TO SEQ ID NO: 2:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 695 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase al (hsGCaI))

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

45

Phe Ser Leu Leu Ala Pro Gly Gln Val Pro Asn Glu Ser Ser Glu Glu
 20 25 30
 Ala Ala Gly Ser Ser Glu Ser Cys Lys Ala Thr Val Pro Ile Cys Gln
 35 40 45

50

Asp Ile Pro Glu Lys Asn Ile Gln Glu Ser Leu Pro Gln Arg Lys Thr
50 55 60

Ser Arg Ser Arg Val Tyr Leu His Thr Leu Ala Glu Ser Ile Cys Lys
 65 70 75 80

55

Leu Ile Phe Pro Glu Phe Glu Arg Leu Asn Val Ala Leu Gln Arg Thr
 85 89 95

1

Leu Ala Lys His Lys Ile Lys Glu Ser Arg Lys Ser Leu Glu Arg Glu
 85 90 95
 100 105 110

Tyr Glu Glu Asp Glu Asn Ile Leu Gly Val Val Gly Gly Thr Leu Lys
 145 150 155 160
 Asp Phe Leu Asn Ser Phe Ser Thr Leu Leu Lys Gln Ser Ser His Cys
 165 170 175
 5 Gln Glu Ala Gly Lys Arg Gly Arg Leu Glu Asp Ala Ser Ile Leu Cys
 180 185 190
 Leu Asp Lys Glu Asp Asp Phe Leu His Val Tyr Tyr Phe Phe Pro Lys
 195 200 205
 Arg Thr Thr Ser Leu Ile Leu Pro Gly Ile Ile Lys Ala Ala Ala His
 10 210 215 220
 Val Leu Tyr Glu Thr Glu Val Glu Val Ser Leu Met Pro Pro Cys Phe
 2225 230 235 240
 His Asn Asp Cys Ser Glu Phe Val Asn Gln Pro Tyr Leu Leu Tyr Ser
 245 250 255
 15 Val His Met Lys Ser Thr Lys Pro Ser Leu Ser Pro Ser Lys Pro Gln
 260 265 270
 Ser Ser Leu Val Ile Pro Thr Ser Leu Phe Cys Lys Thr Phe Pro Phe
 275 280 285
 His Phe Met Phe Asp Lys Asp Met Thr Ile Leu Gln Phe Gly Asn Gly
 20 290 300 305
 Ile Arg Arg Leu Met Asn Arg Arg Asp Phe Gln Gly Lys Pro Asn Phe
 310 315 320 325
 Glu Glu Tyr Phe Glu Ile Leu Thr Pro Lys Ile Asn Gln Thr Phe Ser
 330 335 340
 25 Gly Ile Met Thr Met Leu Asn Met Gln Phe Val Val Arg Val Arg Arg
 345 350 355
 Trp Asp Asn Ser Val Lys Lys Ser Ser Arg Val Met Asp Leu Lys Gly
 360 365 370
 Gln Met Ile Tyr Ile Val Glu Ser Ser Ala Ile Leu Phe Leu Gly Ser
 30 375 380 385
 Pro Cys Val Asp Arg Leu Glu Asp Phe Thr Gly Arg Gly Leu Tyr Leu
 390 395 400 405
 Ser Asp Ile Pro Ile His Asn Ala Leu Arg Asp Val Val Leu Ile Gly
 410 415 420
 35 Glu Gln Ala Arg Ala Gln Asp Gly Leu Lys Lys Arg Leu Gly Lys Leu
 425 430 435
 Lys Ala Thr Leu Glu Gln Ala His Gln Ala Leu Glu Glu Glu Lys Lys
 440 445 450
 40 Lys Thr Val Asp Leu Leu Cys Ser Ile Phe Pro Cys Glu Val Ala Gln
 455 460 465
 Gln Leu Trp Gln Gly Gln Val Val Gln Ala Lys Lys Phe Ser Asn Val
 470 475 480 485
 Thr Met Leu Phe Ser Asp Ile Val Gly Phe Thr Ala Ile Cys Ser Gln
 490 495 500
 45 Cys Ser Pro Leu Gln Val Ile Thr Met Leu Asn Ala Leu Tyr Thr Arg
 505 510 515
 Phe Asp Gln Gln Cys Gly Glu Leu Asp Val Tyr Lys Val Glu Thr Ile
 520 525 530
 50 Gly Asp Ala Tyr Cys Val Ala Gly Gly Leu His Lys Glu Ser Asp Thr
 535 540 545
 His Ala Val Gln Ile Ala Leu Met Ala Leu Lys Met Met Glu Leu Ser
 550 555 560 565
 Asp Glu Val Met Ser Pro His Gly Glu Pro Ile Lys Met Arg Ile Gly
 570 575 580
 55 Leu His Ser Gly Ser Val Phe Ala Gly Val Val Gly Val Lys Met Pro
 585 590 595
 Arg Tyr Cys Leu Phe Gly Asn Asn Val Thr Leu Ala Asn Lys Phe Glu
 600 605 610
 Ser Cys Ser Val Pro Arg Lys Ile Asn Val Ser Pro Thr Thr Tyr Arg
 615 620 625
 Leu Leu Lys Asp Cys Pro Gly Phe Val Phe Thr Pro Arg Ser Arg Glu

630	635	640	645
Glu Leu Pro Pro Asn Phe Pro Ser Glu Ile Pro Gly Ile Cys His Phe			
650	655	660	
Leu Asp Ala Tyr Gln Gln Gly Thr Asn Ser Lys Pro Cys Phe Gln Lys			
665	670	675	
Lys Asp Val Glu Asp Gly Asn Ala Asn Phe Leu Gly Lys Ala Ser Gly			
680	685	690	
Ile Asp			
695			

10

(2) DATA TO SEQ ID NO: 3:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2443 basepairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: doublestrand
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

25	CCCCCCCCCG CCGCTGCCGC CTCTGCCTGG GTCCCTTCGG CCGTACCTCT GCGTGGGGC	60
	TGCCTCCCCG GCTCCCGGTG CAGACACCAT GTACGGATT GTGAATCACG CCCTGGAGTT	120
	GCTGGTGATC CGCAATTACG GCCCCGAGGT GTGGGAAGAC ATCAAAAAAG AGGCACAGTT	180
	AGATGAAGAA GGACAGTTTC TTGTCAGAAT AATATATGAT GACTCCAAA CTTATGATTT	240
	GGTTGCTGCT GCAAGCAAAG TCCTCAATCT CAATGCTGGA GAAATCCTCC AAATGTTGG	300
30	GAAGATGTTT TTCGTCCTTT GCCAAGAACAT TGTTTATGAT ACAATCTTGC GTGTCCTGGG	360
	CTCTAATGTC AGAGAATTTC TACAGAACCT TGATGCTCTG CACGACCACC TTGCTACCAC	420
	CTACCCAGGA ATGCGTGCAC CTTCCCTTAG GTGCACTGAT GCAGAAAAGG GCAAAGGACT	480
	CATTTGCAC TACTACTCAG AGAGAGAAGG ACTTCAGGAT ATTGTCATTG GAATCATCAA	540
	AACAGTGGCA CAACAAATCC ATGGCACTGA AATAGACATG AACGTTTATTG AGCAAAGAAA	600
35	TGAAGAATGT GATCATACTC AATTTTAAT TGAAGAAAAA GAGTCAAAAG AAGAGGATT	660
	TTATGAAGAT CTTGACAGAT TTGAAGAAAAA TGGTACCCAG GAATCACGCA TCAGCCCATA	720
	TACATTCTGC AAAGCTTTTC CTTTCATAT AATATTTGAC CGGGACCTAG TGGTCACTCA	780
	GTGTGGCAAT GCTATATACA GAGTTCTCCC CCAGCTCCAG CCTGGGAATT GCAGCCTTCT	840
	GTCTGTCTTC TCGCTGGTTC GTCCTCATAT TGATATTAGT TTCCATGGGA TCCTTTCTCA	900
40	CATCAATACT GTTTTGTAT TGAGAACCAA GGAAGGATTG TTGGATGTGG AGAAATTAGA	960
	ATGTGAGGAT GAACTGACTG GGACTGAGAT CAGCTGCTTA CGTCTCAAGG GTCAAATGAT	1020
	CTACTTACCT GAAGCAGATA GCATACTTT TCTATGTTCA CCAAGTGTCA TGAACCTGG	1080
	CGATTGACA AGGAGAGGGC TGTATCTAAG TGACATCCCT CTGCATGATG CCACCGCGCA	1140
	TCTTGTCTT TTGGGAGAAC AATTTAGAGA GGAATACAAA CTCACCAAG AACTGGAAAT	1200
45	CCTCACTGAC AGGCTACAGC TCACGTTAAC AGCCCTGGAA GATGAAAAGA AAAAGACAGA	1260
	CACATTGCTG TATTCTGTCC TTCCCTCCGC TGGTGCCTAAT GAGCTGGGC ACAAGCGTCC	1320
	AGTGCCTGCC AAAAGATATG ACAATGTGAC CATCCTCTT AGTGGCATTG TGGGCTTCAA	1380
	TGCTTTCTGT AGCAAGCATG CATCTGGAGA AGGAGCCATG AAGATCGTCA ACCTCCTCAA	1440
	CGACCTCTAC ACCAGATTG ACACACTGAC TGATTCCCGG AAAAACCCAT TTGTTTATAA	1500
	GGTGGAGACT GTTGGTGACA AGTATATGAC AGTGAGTGG TTACCAAGAGC CATGCATTCA	1560
	CCATGCACGA TCCATCTGCC ACCTGGCCTT GGACATGATG GAAATTGCTG GCCAGGTTCA	1620
	AGTAGATGGT GAATCTGTC AGATAACAAT AGGGATAACAC ACTGGAGAGG TAGTTACAGG	1680
	TGTCTAGAGA CAGCGGATGC CTCGATACTG TCTTTTGGG AATACTGTCA ACCTCACAA	1740
	CCGAACAGAA ACCACAGGAG AAAAGGGAAA AATAATGTG TCTGAATATA CATAACAGATG	1800
55	TCTTATGCT CCAGAAAATT CAGATCCACA ATTCCACTTG GAGCACAGAG GCCCAGTGT	1860
	CATGAAGGGC AAAAAAGAAC CAATGCAAGT TTGGTTCTA TCCAGAAAAA ATACAGGAAC	1920
	AGAGGAAACA AAGCAGGATG ATGACTGAAT CTTGGATTAT GGGGTGAAGA GGAGTACAGA	1980
	CTAGGTTCCA GTTTCTCCT AACACGTGCC AAGCCCAGGA GCAGTCTTC CCTATGGATA	2040
	CAGATTTCTT TTTGCTCTTG TCCATTACCC CAAGACTTTTC TTCTAGATAT ATCTCTCACT	2100
60	ATCCGTTATT CAACCTTAGC TCTGCTTTCT ATTACTTTT AGGCTTAGT ATATTATCTA	2160
	AAGTTGGCT TTTGATGTGG ATGATGTGAG CTTCATGTGT CTTAAAATCT ACTACAAGCA	2220

TTACCTAAC	TGGTGATCTG	CAAGTAGTAG	GCACCCAATA	AATATTGTT	GAATTTAGTT	2280
AAATGAAACT	GAACAGTGT	TGGCCATGTG	TATATTATA	TCATGTTAC	CAAATCTGTT	2340
TAGTGTCCA	CATATATGTA	TATGTATATT	TTAATGACTA	TAATGTAATA	AAGTTTATAT	2400
CATGTTGGTG	TATATCATT	TAGAAATCAT	TTTCTAAAGG	AGT		2443

5

(2) DATA TO SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 619 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein (human soluble guanylyl cyclase b1 (hsGcb1))

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 4:

20 Met	Tyr	Gly	Phe	Val	Asn	His	Ala	Leu	Glu	Leu	Leu	Val	Ile	Arg	Asn	
									5	10				15		
	Tyr	Gly	Pro	Glu	Val	Trp	Glu	Asp	Ile	Lys	Lys	Glu	Ala	Gln	Leu	Asp
									20	25				30		
25	Glu	Glu	Gly	Gln	Phe	Leu	Val	Arg	Ile	Ile	Tyr	Asp	Asp	Ser	Lys	Thr
									35	40				45		
	Tyr	Asp	Leu	Val	Ala	Ala	Ala	Ser	Lys	Val	Leu	Asn	Leu	Asn	Ala	Gly
									50	55				60		
30	Glu	Ile	Leu	Gln	Met	Phe	Gly	Lys	Met	Phe	Phe	Val	Phe	Cys	Gln	Glu
									65	70				80		
35	Ser	Gly	Tyr	Asp	Thr	Ile	Leu	Arg	Val	Leu	Gly	Ser	Asn	Val	Arg	Glu
									85	90				95		
	Phe	Leu	Gln	Asn	Leu	Asp	Ala	Leu	His	Asp	His	Leu	Ala	Thr	Ile	Tyr
									100	105				110		
40	Pro	Gly	Met	Arg	Ala	Pro	Ser	Phe	Arg	Cys	Thr	Asp	Ala	Glu	Lys	Gly
									115	120				125		
45	Lys	Gly	Leu	Ile	Leu	His	Tyr	Tyr	Ser	Glu	Arg	Glu	Gly	Leu	Gln	Asp
									130	135				140		
	Ile	Val	Ile	Gly	Ile	Ile	Lys	Thr	Val	Ala	Gln	Ile	His	Gly	Thr	
									145	150				160		
50	Glu	Ile	Asp	Met	Lys	Val	Ile	Gln	Gln	Arg	Asn	Glu	Glu	Cys	Asp	His
									165	170				175		
	Thr	Gln	Phe	Leu	Ile	Glu	Glu	Lys	Glu	Ser	Lys	Glu	Glu	Asp	Phe	Tyr
									180	185				190		
55	Glu	Asp	Leu	Asp	Arg	Phe	Glu	Glu	Asn	Gly	Thr	Gln	Glu	Ser	Arg	Ile
									195	200				205		
	Ser	Pro	Tyr	Thr	Phe	Cys	Lys	Ala	Phe	Pro	Phe	His	Ile	Ile	Phe	Asp
									210	215				220		
	Arg	Asp	Leu	Val	Val	Thr	Gln	Cys	Gly	Asn	Ala	Ile	Tyr	Arg	Val	Leu
									225	230				240		
60	Pro	Gln	Leu	Gln	Pro	Gly	Asn	Cys	Ser	Leu	Leu	Ser	Val	Phe	Ser	Leu
									245	250				255		
	Val	Arg	Pro	His	Ile	Asp	Ile	Ser	Phe	His	Gly	Ile	Leu	Ser	His	Ile
									260	265				270		
	Asn	Thr	Val	Phe	Val	Leu	Arg	Ser	Lys	Glu	Gly	Leu	Leu	Asp	Val	Glu
									275	280				285		
	Lys	Leu	Glu	Cys	Glu	Asp	Glu	Leu	Thr	Gly	Thr	Glu	Ile	Ser	Cys	Leu
									290	295				300		
	Arg	Leu	Lys	Gly	Gln	Met	Ile	Tyr	Leu	Pro	Glu	Ala	Asp	Ser	Ile	Leu
									305	310				315		
	Phe	Leu	Cys	Ser	Pro	Ser	Val	Met	Asn	Leu	Asp	Asp	Leu	Thr	Arg	Arg
									325	330				335		

	Gly	Leu	Tyr	Leu	Ser	Asp	Ile	Pro	Leu	His	Asp	Ala	Thr	Arg	Asp	Leu
							340		345					350		
	Val	Leu	Leu	Gly	Glu	Gln	Phe	Arg	Glu	Glu	Tyr	Lys	Leu	Thr	Gln	Glu
							355		360					365		
5	Leu	Glu	Ile	Leu	Thr	Asp	Arg	Leu	Gln	Leu	Thr	Leu	Arg	Ala	Leu	Glu
							370		375					380		
	Asp	Glu	Lys	Lys	Lys	Thr	Asp	Thr	Leu	Leu	Tyr	Ser	Val	Leu	Pro	Pro
							385		390					395		400
10	Ser	Val	Ala	Asn	Glu	Leu	Arg	His	Lys	Arg	Pro	Val	Pro	Ala	Lys	Arg
							405		410					415		
	Tyr	Asp	Asn	Val	Thr	Ile	Leu	Phe	Ser	Gly	Ile	Val	Gly	Phe	Asn	Ala
							420		425					430		
	Phe	Cys	Ser	Lys	His	Ala	Ser	Gly	Glu	Gly	Ala	Met	Lys	Ile	Val	Asn
							435		440					445		
15	Leu	Leu	Asn	Asp	Leu	Tyr	Thr	Arg	Phe	Asp	Thr	Leu	Thr	Asp	Ser	Arg
							450		455					460		
	Lys	Asn	Pro	Phe	Val	Tyr	Lys	Val	Glu	Thr	Val	Gly	Asp	Lys	Tyr	Met
							465		470					475		480
20	Thr	Val	Ser	Gly	Leu	Pro	Glu	Pro	Cys	Ile	His	His	Ala	Arg	Ser	Ile
							485		490					495		
	Cys	His	Leu	Ala	Leu	Asp	Met	Met	Glu	Ile	Ala	Gly	Gln	Val	Gln	Val
							500		505					510		
	Asp	Gly	Glu	Ser	Val	Gln	Ile	Thr	Ile	Gly	Ile	His	Thr	Gly	Glu	Val
							515		520					525		
25	val	Thr	Gly	Val	Ile	Gly	Gln	Arg	Met	Pro	Arg	Tyr	Cys	Leu	Phe	Gly
							530		535					540		
	Asn	Thr	Val	Asn	Leu	Thr	Ser	Arg	Thr	Glu	Thr	Thr	Gly	Glu	Lys	Gly
							545		550					555		560
30	Lys	Ile	Asn	Val	Ser	Glu	Tyr	Thr	Tyr	Arg	Cys	Leu	Met	Ser	Pro	Glu
							565		570					575		
	Asn	Ser	Asp	Pro	Gln	Phe	His	Leu	Glu	His	Arg	Gly	Pro	Val	Ser	Met
							580		585					590		
	Lys	Gly	Lys	Lys	Glu	Pro	Met	Gln	Val	Trp	Phe	Leu	Ser	Arg	Lys	Asn
							595		600					605		
35	Thr	Gly	Thr	Glu	Glu	Thr	Lys	Gln	Asp	Asp	Asp					
							610		615							

(2) DATA TO SEQ ID NO: 5:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: peptide (amino acids 634-647 of hsGCal)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

50 Phe Thr Pro Arg Ser Arg Glu Glu Leu Pro Pro Asn Phe Pro
 5 10

(2) DATA TO SEQ ID NO: 6:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 60 (ii) MOLECULE TYPE: peptide (amino acids 593-614 of hsGCb1)

(xi) SEQUENCEDESCRIPTION: SEQ ID NO: 6:

5 Lys Gly Lys Lys Glu Pro Met Gln Val Trp Phe Leu Ser Arg Lys Asn
5 10 15
Thr Gly Thr Glu Glu Thr
20

10 (2) DATA TO SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 basepairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single strands
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: genomic DNA

20 (iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

25 (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 7:

AAAAGGATCC ATGTTCTGCA CGAAGCTC

28

30 2) DATA TO SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 basepairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single strands
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: genomic DNA

40 (iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

45 (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 8:

50 ATTATGGAAG CAGGGAGG

18

55 2) DATA TO SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 basepairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single strands
- (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: genomic DNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

5 (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 9:

AAAAGGATCC ATGTACGGAT TTGTGAAT

28

10 2) DATA TO SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 basepairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single strands
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

20 (iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

25 (xi) SEQUENCEDESCRIPTION: SEQ ID NO: 10:

ATGCGTGATT CCTGGGTACC

20